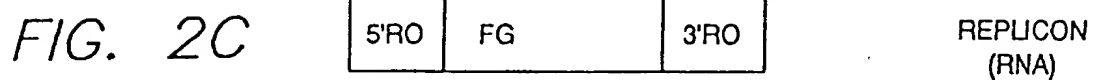
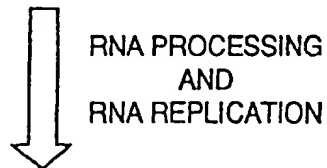
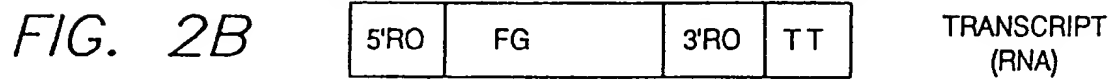
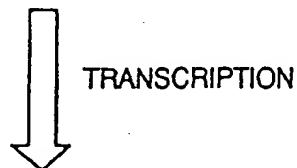
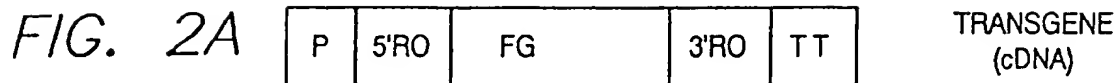


- GENOMIC RNA
- ◆ AMBER STOP CODON (READTHROUGH SITE)
- SUBGENOMIC PROMOTER
- SUBGENOMIC mRNA
- ↑↓ TRANSLATION
- ▣ VIRAL PROTEIN
- REPLICATION ORIGINS
- R REPLICASE PROTEINS
- M MOVEMENT PROTEIN
- C CAPSID PROTEIN
- 1 cm ~ 0.6 kb

FIG. 1

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P = PROMOTER

5'RO = 5' REPLICATION ORIGIN

FG = SEQUENCE CODING FOR FOREIGN GENE AS WELL AS OTHER SEQUENCES.  
DOES NOT CODE FOR COMPLETE SET OF VIRAL REPLICATION PROTEINS  
REQUIRED FOR REPLICATION.

3' RO = 3' REPLICATION ORIGIN

TT = TRANSCRIPTION TERMINATION SEQUENCE

*FIG. 2*

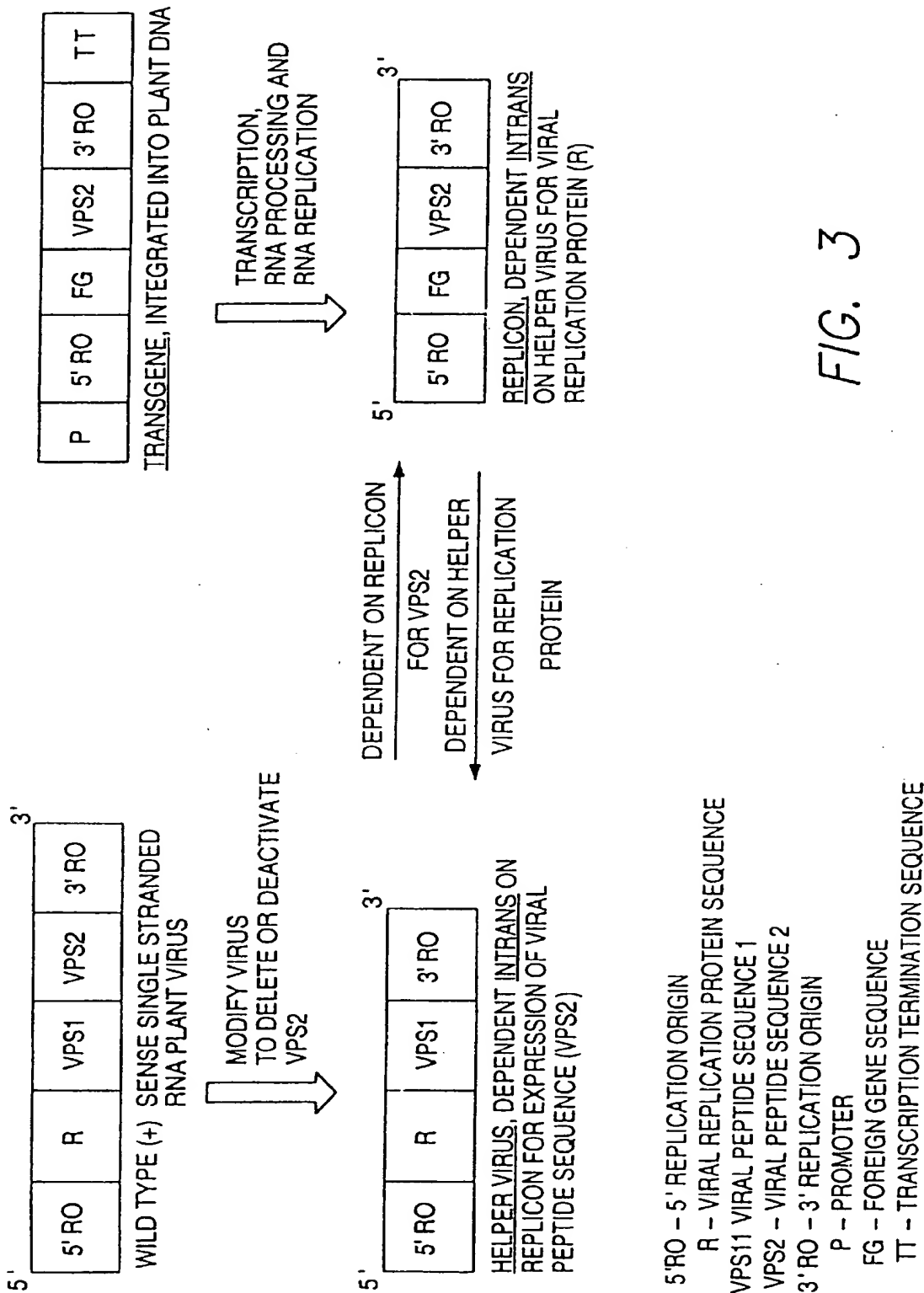


FIG. 3

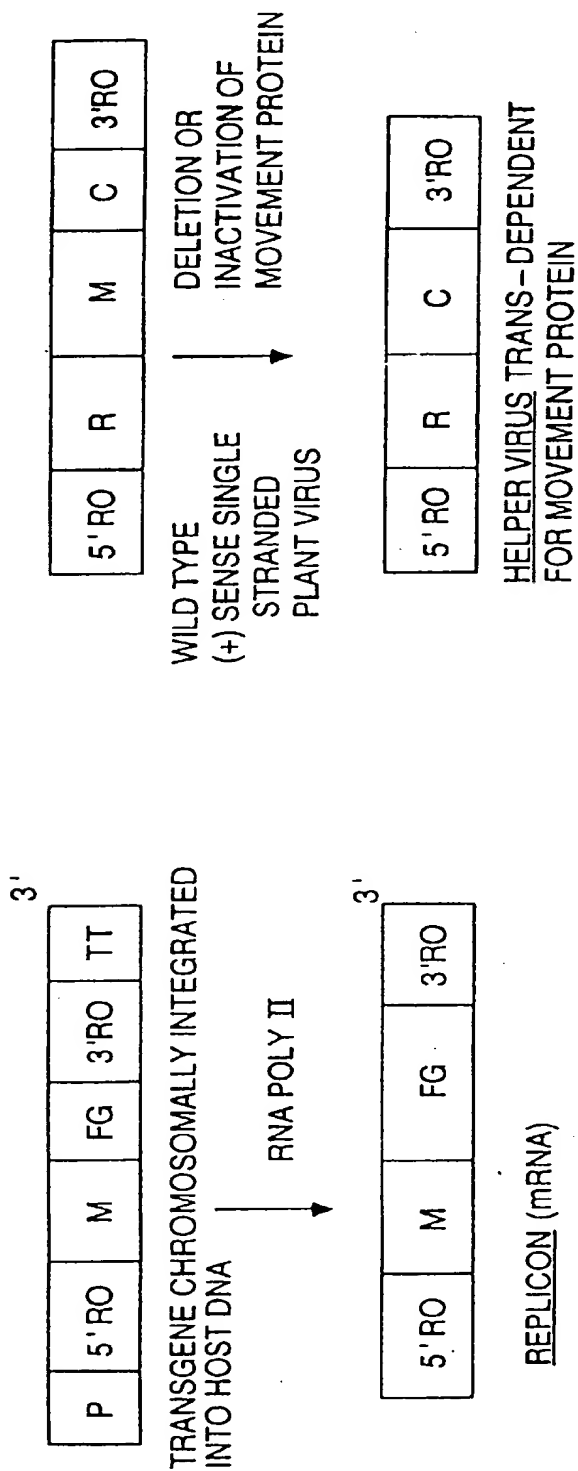


FIG. 4

R: REPLICATION PROTEINS GENES  
M: MOVEMENT PROTEIN GENE  
RO: REPLICATION ORIGIN  
RT: RIBOZYME TERMINATION REGION  
CAT: CHLORAMPHENICOL ACETYL TRANSFERASE  
P: 35S PROMOTER

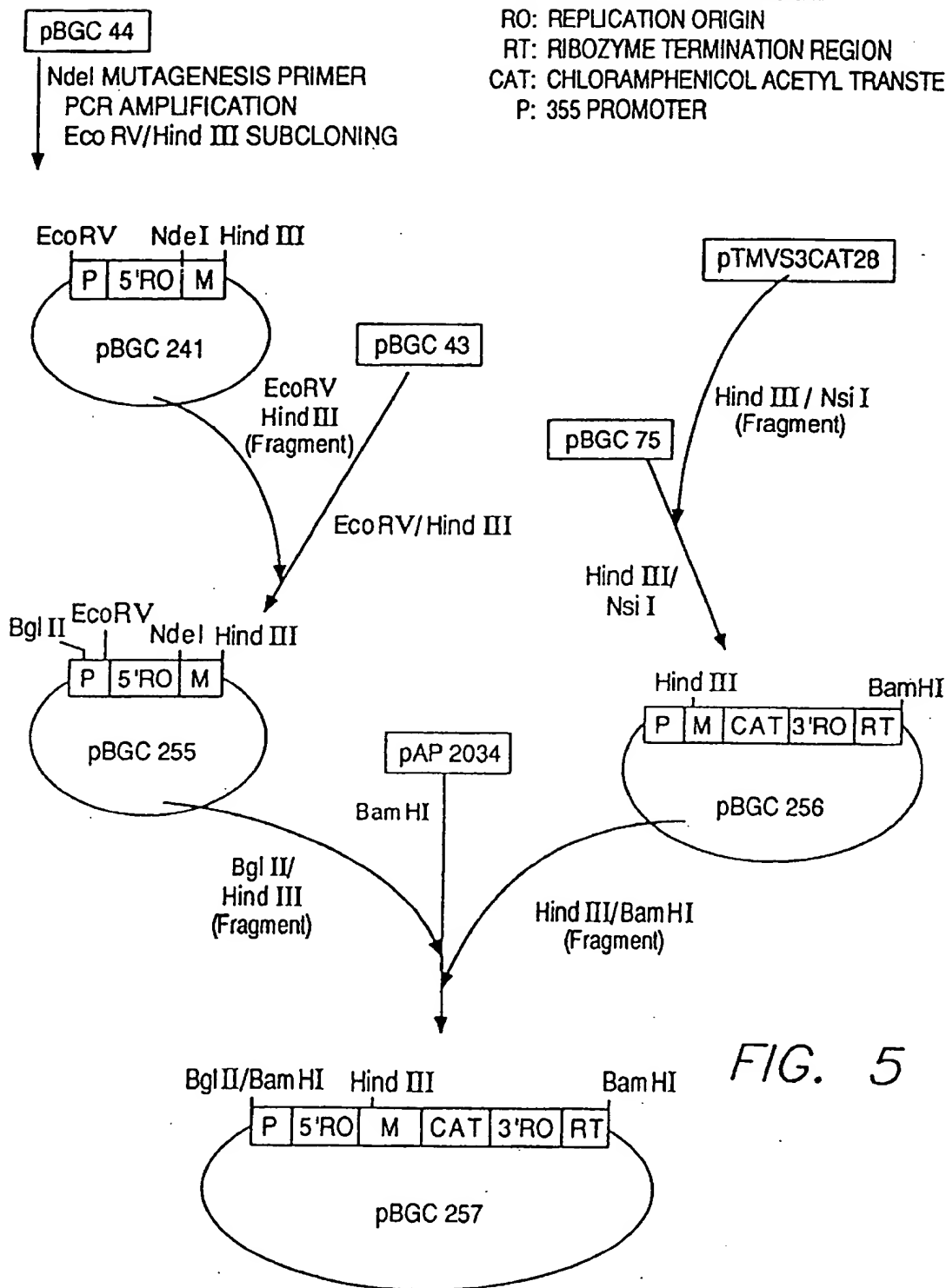


FIG. 5

1	guuuuuuuacaacaauuacaaacaacaacaacaacaacaacaauuacauuuu	60
61	cauuuacau AUG GCU CUA GUU GUU AAA GGA AAA GUG AAU AUC AAU	105
1	M A L V V K G K V N I N	12
5		
106	GAG UUU AUC GAC CUG ACA AAA AUG GAG AAG AUC UUA CCG UCG AUG	150
13	E F I D L T K M E K I L P S M	27
151	UUU ACC CCU GUA AAG AGU GUU AUG UGU UCC AAA GUU GAU AAA AUA	195
28	F T P V K S V M C S K V D K I	42
196	AUG GUU CAU GAG AAU GAG UCA UUG UCA GAG GUG AAC CUU UUU AAA	240
43	M V H E N E S L S E V N L L K	57
241	GGA GUU AAG CUU AUU GAU AGU GGA UAC GUC UGU UUA GCC GGU UUG	285
58	G V K L I D S G Y V C L A G L	72
286	GUC GUC ACG GGC GAG UGG AAC UUG CCU GAC AAU UGC AGA GGA GGU	330
73	V V T G E W N L P D N C R G G	87
331	GUG AGC GUG UGU CUG GUG GAC AAA AGG AUG GAA AGA GCC GAC GAG	375
88	V S V C L V D K R M E R A D E	102
376	GCC ACU CUC GGA UCU UAC UAC ACA GCA GCU GCA AAG AAA AGA UUU	420
103	A T L G S Y Y T A A A K K R F	117
421	CAG UUC AAG GUC GUU CCC AAU UAU GCU AUA ACC ACC CAG GAC GCG	465
118	Q F K V V P N Y A I T T Q D A	132
466	AUG AAA AAC GUC UGG CAA GUU UUA GUU AAU AUU AGA AAU GUG AAG	510
133	M K N V W Q V L V N I R N V K	147
511	AUG UCA GCG GGU UUC UGU CCG CUU UCU CUG GAG UUU GUG UCG GUG	555
148	M S A G F C P L S L E F V S V	162
556	UGU AUU GUU UAU AGA AAU AAU AUA AAA UUA GGU UUG AGA GAG AAG	600
163	C I V Y R N N I K L G L R E K	177
601	AUU ACA AAC GUG AGA GAC GGA GGG CCC AUG GAA CUU ACA GAA GAA	645
178	I T N V R D G G P M E L T E E	192
646	GUC GUU GAU GAG UUC AUG GAA GAU GUC CCU AUG UCG AUC AGG CUU	690
193	V V D E F M E D V P M S I R L	207
691	GCA AAG UUU CGA UCU CGA ACC GGA AAA AAG AGU GAU GUC CGC AAA	735
208	A K F R S R T G K K S D V R K	222

FIG. 6-2

	736	GGG	AAA	AAU	AGU	AGU	AAU	GAU	CGG	UCA	GUG	CCG	AAC	AAG	AAC	UAU	780
	233	G	K	N	S	S	N	D	R	S	V	P	N	K	N	Y	237
50																	
	781	AGA	AAU	GUU	AAG	GAU	UUU	GGA	GGA	AUG	AGU	UUU	AAA	AAG	AAU	AAU	825
	238	R	N	V	K	D	F	G	G	M	S	F	K	K	N	N	252
	826	UUA	AUC	GAU	GAU	GAU	UCG	GAG	GCU	ACU	GUC	GCC	GAA	UCG	GAU	UCG	870
	253	L	I	D	D	D	S	E	A	T	V	A	E	S	D	S	267
5																	
	871	UUU	UAA	auacgcucgacgagauuuucaggagcuaaggaagcuaaa										AUG	GAG	AAA	924
	263	F	*											M	E	K	3
	925	AAA	AUC	ACU	GGA	UAU	ACC	ACC	GUU	GAU	AUA	UCC	CAA	UCG	CAU	CGU	969
	4	K	I	T	G	Y	T	T	V	D	I	S	Q	S	H	R	18
10																	
	970	AAA	GAA	CAU	UUU	GAG	GCA	UUU	CAG	UCA	GUU	GCU	CAA	UGU	ACC	UAU	1014
	19	K	E	H	F	E	A	F	Q	S	V	A	Q	C	T	Y	33
																	C
																	A
																	T
15																	
	1015	AAC	CAG	ACC	GUU	CAG	CUG	GAU	AUU	ACG	GCC	UUU	UUA	AAG	ACC	GUA	1059
	34	N	Q	T	V	Q	L	D	I	T	A	F	L	K	T	V	48
																	P
																	R
	1060	AAG	AAA	AAU	AAG	CAC	AAG	UUU	UAU	CCG	GCC	UUU	AUU	CAC	AUU	CUU	1104
	49	K	K	N	K	H	K	F	Y	P	A	F	I	H	I	L	63
																	O
																	T
																	E
20																	
	1105	GCC	CGC	CUG	AUG	AAU	GCU	CAU	CCG	GAA	UUC	CGU	AUG	GCA	AUG	AAA	1149
	64	A	R	L	M	N	A	H	P	E	F	R	M	A	M	K	78
																	N
	1195	GUU	UUC	CAU	GAG	CAA	ACU	GAA	ACG	UUU	UCA	UCG	CUC	UGG	AGU	GAA	1239
	94	V	F	H	E	Q	T	E	T	F	S	S	L	W	S	E	108
25																	
	1240	UAC	CAC	GAC	GAU	UUC	CGG	CAG	UUU	CUA	CAC	AUA	UAU	UCG	CAA	GAU	1284
	109	Y	H	D	D	F	R	Q	F	L	H	I	Y	S	Q	D	123
	1285	GUG	GCG	UGU	UAC	GGU	GAA	AAC	CUG	GCC	UAU	UUC	CCU	AAA	GGG	UUU	1329
30	124	V	A	C	Y	G	E	N	L	A	Y	F	P	K	G	F	138
	1330	AUU	GAG	AAU	AUG	UUU	UUC	GUC	UCA	GCC	AAU	CCC	UGG	GUG	AGU	UUC	1374
	139	I	E	N	M	F	F	V	S	A	N	P	W	V	S	F	153
35																	
	1375	ACC	AGU	UUU	GAU	UUA	AAC	GUG	GCC	AAU	AUG	GAC	AAC	UUC	UUC	GCC	1419
	154	T	S	F	D	L	N	V	A	N	M	D	N	F	F	A	168
	1420	CCC	GUU	UUC	ACC	AUG	GGC	AAA	UAU	UAU	ACG	CAA	GGC	GAC	AAG	GUG	1464
	169	P	V	F	T	M	G	K	Y	Y	T	Q	G	D	K	V	183
40																	

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FIG. 6-3

	1465	CUG	AUG	CCG	CUG	GCG	AUU	CAG	GUU	CAU	CAU	GCC	GUC	UGU	GAU	GGC	1509
	184	L	M	P	L	A	I	Q	V	H	H	A	V	C	D	G	198
	1510	UUC	CAU	GUC	GGC	AGA	AUG	CUU	AAU	GAA	UUA	CAA	CAG	UAC	UGC	GAU	1554
45	199	F	H	V	G	R	M	L	N	E	L	Q	Q	Y	C	D	213
	1555	GAG	UGG	CAG	GGC	GGG	GCG	UAA	uuuuuuu	aaggc	aguuau	uggug	cccu	aaaac			1607
	214	E	W	Q	G	G	A	*									220 ↓
	1608	gcc	uggug	cuac	gcc	cuga	aua	agug	aua	uaag	cgg	aug	aaug	gcag	aaau	ucguc	gagg 1667
50	1668	guag	uca	aag	aug	cau	aa	uaa	aa	uaac	ggau	ugug	uccg	uauc	acac	cgugg	ugcguacgau 1727
	1728	aac	gau	agug	uuuu	uccc	ucc	acuu	aaa	auc	gaag	ggug	uguc	uugg	aucg	cgcg	ggguc 1787
	1788	aaa	guau	augg	uuca	ua	uac	aucc	gcag	gcac	gua	aua	aaag	cga	gggu	ucgaa	uccc 1847
	1848	ccg	uuac	cccc	cggu	aggg	ggcca										1870

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